AMENDMENTS TO THE CLAIMS

Listing of Claims

1. (Currently Amended) A method for analysing the metabolites of a first biological sample which comprises quantitatively determining at least 50 ~~one or more~~ metabolites in said first sample in a way that said quantitative determination resolves isotopic mass differences within each ~~one~~ metabolite, said method comprising ~~being characterized in that the sample comprises or is derived from a cell~~

a) taking a first biological sample from cells which have been maintained under conditions allowing the uptake of an isotopically labeled metabolizable compound in which substantially all atoms of a given element are isotopically labelled so that the metabolites in said cells are saturated with the isotope with which said metabolizable compound is labeled, wherein the proportion of the label-isotope of at least 50 metabolites of the biological sample is increased to at least 80% of the total of all isotopes of the element;

(b) combining said first biological sample with a second biological sample in which the metabolites are not isotopically labelled or are isotopically labelled differently from the first biological sample;

(c) separating the metabolites in the samples chromatographically;

(d) quantitatively determining at least 50 of the metabolites separated in (c) by mass spectrometry;

(e) obtaining for each quantitatively determined metabolite a matrix of

(i) chromatographic retention time,

(ii) mass, and

(iii) signal strength;

(f) calculating for each quantitatively determined metabolite of the first and the second sample an isotopomer ratio (ITR) on the basis of the measured signal strengths;

wherein the at least 50 metabolites comprise sugars, sugar alcohols, organic acids, amino acids, fatty acids, vitamins, sterols, phosphates, polyamines, polyols, nucleosides, adenine, ethanolamine, nicotinic acid, uracil and/or urea.

2. (Cancelled)

3. (Currently Amended) The method of claim 1 [[2]], wherein the first and the second biological sample correspond to different phenotypic and/or genotypic states of the cells comprised in the samples or from which the samples are derived.

4. (Original) The method of claim 3, wherein the different phenotypic and/or genotypic states are different developmental stages, environments, nutritional supplies, taxonomic units, wild-type and mutant or transgenic genomes, infected and uninfected states, diseased and healthy states or different stages of a pathogenicity.

5. (Cancelled)

6. (Cancelled)

7. (Previously Presented) The method of claim 1, wherein the isotope is ^{13}C, ^{15}N, ^{18}O or ^{2}H.

8. (Original) The method of claim 7, wherein the isotopically labeled metabolizable compound is U-^{13}C-glucose, $^{2}H_2O$, $H_2{}^{18}O$, U-^{13}C acidic acid, ^{13}C carbonate or ^{13}C carbonic acid.

9. (Previously Presented) The method of claim 1, wherein the biological sample comprises yeast cells or plant cells.

10. (Cancelled)

11. (Cancelled)

12. (Currently Amended) The method of claim 1 [[11]], wherein mass spectrometry is MALDI-TOF.

13. (Cancelled)

14. (Previously Presented) The method of claim 1, further comprising the step of introducing external standards for one or more of the quantitatively determined metabolites.

15. (Currently Amended) The method of claim 1, further comprising the step of identifying ~~one or more of~~ the metabolites which are quantitatively determined.

16. (Original) The method of claim 15, wherein said metabolites are identified by secondary fragmentation.

17. (Original) The method of claim 16, wherein identifying of said metabolites comprises electron impact ionisation, MS-MS technology and/or post source decay analyses of molecular ions or fragments.

18. (Cancelled)

19. (Cancelled)

20. (Previously Presented) The method of claim 1, wherein, in addition to metabolites, one or more proteins and/or RNA transcripts in said sample are quantitatively determined and analysed.

21. (Cancelled)

22. (Previously Presented) The method of claim 1, wherein said analysing further involves suitable statistical evaluation and correlation analyses of the data obtained and, optionally, network analyses.

23. (Original) A set of isotopically labeled metabolites obtainable from a sample which comprises or is derived from a cell which has been maintained under conditions allowing the uptake of an isotopically labeled metabolizable compound so that the metabolites in said cell are saturated with the isotope with which said metabolizable compound is labeled.

24. (Cancelled)

25. (Previously Presented) A kit comprising an isotopically labeled metabolizable compound and a manual for use in carrying in out the method of claim 1.

26.-28. (Cancelled)

29. (Previously Presented) A kit comprising the set of isotopically labeled metabolites of claim 23.

30. (Cancelled)